

composition in *Brassicaceae* or *Helianthus* seeds and wherein said sequence includes said at least one mutation.

5. (Amended) The nucleic acid fragment of claim [4] 1, wherein said at least one mutation [comprises] in said gene introduces a non-conservative amino acid substitution in said [region] motif.

6. (Amended) The nucleic acid fragment of claim 5, wherein said motif comprises the wild-type amino acid sequence His-Glu-Cys-Gly-His.

7. (Amended) The nucleic acid fragment of claim 6, wherein said at least one mutation in said motif comprises the sequence His-Lys-Cys-Gly-His.

10. (Amended) The nucleic acid fragment of claim [1] 66, wherein said [at least] at least one mutation in said motif comprises the sequence [Lys-]Tyr-His-Asn-Asn-Pro.

27. (Amended) An isolated nucleic acid fragment comprising a sequence of at least about 20 nucleotides from a *Brassicaceae* or *Helianthus* delta-15 fatty acid desaturase gene having at least one mutation in a region of said desaturase gene encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said at least one mutation is effective for altering fatty acid composition in *Brassicaceae* or *Helianthus* seeds and wherein said sequence includes said at least one mutation.

32. (Amended) The nucleic acid fragment of claim 31, wherein said motif comprises the wild-type amino acid sequence His-Asp-Cys-Gly-His.

35. (Amended) A *Brassicaceae* or *Helianthus* plant containing a full-length coding sequence of [at least 20 nucleotides from] a delta-15 fatty acid desaturase gene having at

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least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif and wherein said mutation confers an altered fatty acid composition in seeds of said plant.

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40. (Amended) The plant of claim 39, wherein said motif comprises the wild-type amino acid sequence His-Asp-Cys-Gly-His.

44. (Amended) A *Brassicaceae* or *Helianthus* plant containing:

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a) a full-length coding sequence [of at least 20 nucleotides] from a delta-12 fatty acid desaturase gene having at least one mutation, said at least one delta-12 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and

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b) a full-length coding sequence [of at least 20 nucleotides] from a delta-15 fatty acid desaturase gene having at least one mutation, said at least one delta-15 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; [and

c)] wherein said delta-12 gene mutation and said delta-15 gene mutation confer[ring] an altered fatty acid composition in seeds of said plant.

45. (Amended) The plant of claim 44, wherein said mutant genes confer a decreased level of α -linolenic acid in said seeds compared to α -linolenic acid levels in corresponding seeds lacking said mutant genes.

46. (Amended) A *Brassicaceae* or *Helianthus* plant containing a full-length coding sequence of [at least 20 nucleotides from] a delta-12 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a Tyr-Leu-Asn-Asn-Pro amino acid motif and wherein said